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1/22

1 10 20 30
 NEP1-HU MGK.....SESQMDITDINT..PKPKKKQRWTPLEI.....SLSVLVLLL
 * * * * *
 PEX-HUM MEA.....ETG....SSVET..GKKANRGTRIALVV.....FVGGTLVLG
 * * * * *
 KELL-HU MEGGDQSEEEPRERSQAGGMGTLSQESTPEERLPVEGSRPWAV....ARRVLTAILIL.
 * * * * *
 ECE1-HU MSTYKRATLDEEDLVDSLSEGDAYPNGLQVNFHSPRSGQRCWAARTQVEKRLVVLVLLA
 * * * * *
 consens M T P L

40 50 60 70 80 90
 NEP1-HU TIIAVTMIALYA.TYDD...GICKSSDCIKSAARLIQNMDATTEPCTDFFKYACGGWLKR
 * * * * *
 PEX-HUM TILFLVSQGLLSLQAKQ...EYCLKPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISN
 * * * * *
 KELL-HU .GLLLCFSVLLFYNFQNCGRPPECETSVCLDLRDHYLASGNTSVAPCTDFFSEACG...RA
 * * * * *
 ECE1-HU AGLVACLAALGI.QYQTRSPSVCLSEACVSVTSSILSSMDPTVDPCHDFFSYACGGWIK
 * * * * *
 consens L L C C L V PC DFF ACGGW

100 110 120 130 140 150
 NEP1-HU NVIPETSSRYGNFDILRDELEVVLKDVLPQEP..KTEDIVAVQKAKALYRSCINESAIDSR
 * * * * *
 PEX-HUM NPIPEDMPSYGVYPWLRHNVDLKLEKLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKA
 * * * * *
 KELL-HU KETNNS.....FQELATKNKNRLRRILEVQ.NSWHPGSGEEKAFQFYNSCMDTLAIEAA
 * * * * *
 ECE1-HU NPVPDGHRSRWGTFSNLWEHNQAIKHLLENS.TA.SVSEAERKAQVYRACMNETRIEEL
 * * * * *
 consens N P G F L LK LE A KA Y SCMNE AIE

160 170 180 190 200
 NEP1-HU GGEPLKLLPDI.YGWP..VATENWEQKYGAS.WTAEKAIQNLNSKYGKKVLINLFGVTD
 * * * * *
 PEX-HUM DAKPLLHILRHSPFRWPVLESNIGPEGVWSEKFSLLQTLATFRGQYSNSVFIRLYVSPD
 * * * * *
 KELL-HU GTGPLRQVIEEL.....GGWRISGKWTSLNFN..RTLRLMSQYGHFFFRAYLGPH
 * * * * *
 ECE1-HU RAKPLMELIERL.....GGWNITGPWAKDNFQ..DTLQVVTAHYRTSPFFSVYVSAD
 * * * * *
 consens PL G W F TL Y F YV D

220 230 240 250 260
 NEP1-HU DKNSVNHVIHIDQPRGLPSR.DYECTGIYKEACTAYVDFMISVARLIRQEERLPI.DE
 * * * * *
 PEX-HUM DKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVL.....LGA.NS
 * * * * *
 KELL-HU PASPHTPVIQIDQPEFDVPLKQDQEQKI.YAQIFRE.YLTYLNQLGTL.....LGG.DP
 * * * * *
 ECE1-HU SKSNSNVIQVDQSGGLPSRDYYLNKTENEKVLTG.YLNYMVQLGKL.....LGGGDE
 * * * * *
 consens K S VI DQ L LP R DY K Y M L LG D

111111

00913329.000101

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270 280 290 300 310 320
 NEP1-HU NQLALEMNKVMLEKEIANATAKPEDRNDPMLLYNKMTLAQIQNNFSLEINGKPFPSWLNF
 * * * * *
 PEX-HUM SRAEHDMKSVLRLLEIKIAEIMIPHENRTSEAMY.NKMNISELSAMIP.....QFDWLGY
 * * * * *
 KELL-HU SKVQEHSSLSISITSRLFQFLRPLEQRRAGKLFQMVTIDQLKEMAP.....AIDWLSC
 * * * * *
 ECE1-HU EAIRPQMQQILDFTALANITIPQEKRRDEELIYHKVTAAELQTLAP.....AINWLPF
 * * * * *
 consens M E A P E R K T L P WL

330 340 350 360 370 380
 NEP1-HU TNEIMSTVNISITNEEDVVVYA....PEYLTCLKPILTKYSARDLQNLMSWRFIMDLVSS
 * * * * *
 PEX-HUM IKKVIDTRLYPHLKDIPSENVVVRVPQYFKDLFRILGSEKKTIANYLWVRMVYSRI PN
 * * * * *
 KELL-HU LQATFTPMSLSPSQSLVVHDVEYL...KNMSQLVVEMLLKQRDFLQSHMILGLVVTLSPA
 * * * * *
 ECE1-HU LNTIFYPVEINESEPIVVYDKEYL...EQISTLINT...TDRCLLNNYMIWNLVKRTSSSF
 * * * * *
 consens V L L N M W V

390 400 410 420 430
 NEP1-HU LSRTYKESR....NAFRKALYGT.T.SETATWRRCANVNGNMENAVGRLYVEAAFAGESK
 * * * * *
 PEX-HUM LSRRFQYRW....LEFSRVIQGT.T.TLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKK
 * * * * *
 KELL-HU LDSQFQEARRLKSQKLRELTEQPPMPARPRWMKCVEETGTFFFEPTLAALFVREAFGPSTR
 * * * * *
 ECE1-HU LDQRFQDA....DEKFMEVMYGTKKTCLPRWKFCVSDTENNLGFALGPMFVKATFAEDSK
 * * * * *
 consens L FQ F GT P W CV G FV F K

440 450 460 470 480 490
 NEP1-HU HVVEDLIAQIREVFITLD.DLTWMDAETKRAEEKALAIKERIGYPDDIVSNDNKLNNE
 * * * * *
 PEX-HUM EMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPE.FIMNDTHVNED
 * * * * *
 KELL-HU SAAMKLFTAIRDALITRLR.NLPWMNEETONMAQDKVAQLQVEMGASE.WALKPELARQE
 * * * * *
 ECE1-HU SIATEIILEIKKAFFESLS.TLKWMDEETPKSAKEKADAIYNMIGYPN.FIMDPKELDKV
 * * * * *
 consens L IR AFI L L WMD ET A EKA A GYP
 (4) →
 (1A/B) →

500 510 520 530 540 550
 NEP1-HU YLELNKEDYFENIIQNLFKSQSKQLKKLREKVDKDEWISGAADVNAFYSSGRNQIVFP
 * * * * *
 PEX-HUM LKAIFSEADYFGNVLQTRKYLAQSDFFWLRAVPKTEWFTNPTTVNAFYASTNQIRFP
 * * * * *
 KELL-HU YND.IQLGSSFLQSVLSCVRSRLRARIQSFLOPHQPQRWVSPWDVNAYYSVDHVVFP
 * * * * *
 ECE1-HU FNDYTAVPDLYFENAMRFFNFVSWRVTAQDLRKAPNRDQWSMTPPMVNAYYSPTKNEIVFP
 * * * * *
 consens YF N LR W P VNA YS N IVFP
 (2A/B)

1 (cont'd)

0913329-082101
 1012280-6221650

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	560	570	580	590	600	610
NEP1-HU	AGILQPPFFSAQQ.SNSLNYGGIGMVIGHEITHGFDDNGRNFNKGDLVDWWTQQSASNF					
PEX-HUM	AGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDDNNGRKYDKNGNLDPPWWSTEESEKF					
KELL-HU	AGLLQPPFFHPGY.PRAVNFGAAGSIMAHELLHIFYQL...LLPGGCL....ACDNHAL					
ECE1-HU	AGILQAPFYTRSS.PKALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPWWKNSSVEAF					
consens	AG LQ PFF	P L N G I G	G H E T H F D	G R	K G L W W	S F

	620	630	640	650	660	670
NEP1-HU	KEQSQCMVYQYGNFSWDLAGGQHLNGINTLGENIADNGGGLGQAYRAYQNYI..KKNNG.EE					
PEX-HUM	KEKTKCMINQYSNYWK.KAGLNVKGKRTLGENIADNGGGLREAFRAYRKWINDRRQGLEE					
KELL-HU	QEAHLCLKRHYAAF..PLPSRTSFNDSLTFLENAADVGGGLAIALQAYSRL..LRHH.GE					
ECE1-HU	KRQTECMVEQYSNY..SVNG.EPVNGRHTLGENIADNGGGLKAAYRAYQNWV..KKNNG.AE					
consens	KE CM QY N		NG	TLGENIADNGGGL	A RAY	G E

	680	690	700	710	720	730
NEP1-HU	KLLPGLDLNHNKQLFFLNFAQVWCYTYPYAVNSIKTDVHSPGNFRIIGTLQNSAEFSEA					
PEX-HUM	PLLPGITFTNNQLFFLSYAHVRCNSYRPEAREQVQIGAHSPQFRVNGAISNFEEFQKA					
KELL-HU	TVLPSLDLSPQQIIFRSYAQVMCRKPSQDHS....DTHSPPHLRVHGPLSSTPAFARY					
ECE1-HU	HSLPTLGLTNNQLFFLGFAQVWCSVRTPESSHEGLITDPHSPSRFRVIGSLSNSKEFSEH					
consens	LP L L QLFFL AQV C	PE		D HSP	FRV G LSN	EF

	740	750
NEP1-HU	FHCRKNSYMPNPEKK.CRVW	
PEX-HUM	FNCPPNSTMNRGMDSCRLW	
KELL-HU	FRCARGALLNPSSR.CQLW	
ECE1-HU	FRCPPGSPMNPCHK.CEVW	
consens	F C S MNP	C W

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PRIMER	SEQUENCE
(1A)	5'-TGGATGGAT/CGA/CIGG/AIACIA/CA-3'
(1B)	5'-TGGATGGAT/CGA/CIGG/AIACIA/CG-3'
(2A)	5'-A/GTIGTITTT/CCCIGCIGGIA/GT/AIC/TTA/TCA-3'
(2B)	5'-A/GTIGTITTT/CCCIGCIGGIA/GT/AIC/TTG/CCA-3'
(3)	5'-AIICCICCIA/TC/TA/GTCIGCIG/AC/TA/GTTT/CTC-3'
(4)	5'-GAT/CAAT/CT/CTIGAT/CGAA/GT/CTIAAT/CTGGATGG-3'
(5)	5'-T/CT/CACCAIATICT/GA/GCATCG/TT/CTTCATIGGG/ATG-3'

2017

Sequence of NL-1 cDNA from mouse

[illegible][illegible]

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ala thr met leu arg lys asp gln asn leu ser lys glu ser ala met val arg glu glu met ala glu val leu glu leu glu thr his
811 GCC ACT ATG CTT AGG AAA GAC CAG AAC CTG TCC AAG GAG AGC GCC ATG GTG CGG GAG GAG ATG CCG GAG GTG GAA CTG GAG ACG CAT
leu ala asn ala thr val pro gln glu lys arg his asp val thr ala leu tyr his arg met asp leu met glu leu gln glu arg phe
901 CTG GCC AAC GCC ACA GTC CCC CAG CAG AAA AGG CAT GAT GTC ACT GCC CTG TAC CAC CGA ATG GAC CTG ATG GAG CTA CAG GAA AGG TTT
gly leu lys gly phe asn trp thr leu phe ile gln asn val leu ser ser val glu val glu leu phe pro asp glu glu val val
991 GGT CTG AAG GGG TTT AAC TGG ACT CTC TTC ATA CAA AAC GTG TTG TCT TCT GTG GAA GTC GAG CTG TTC CCA GAT GAG GTG GTG GTC
tyr gly ile pro tyr leu glu asn leu glu asp ile ile asp ser tyr ser ala arg thr met gln asn tyr leu val trp arg leu val
1081 TAC GCC ATC CCC TAC CTG GAG AAT CTG GAG GAT ATC ATT GAT ACC TAC TCA GCA CGG ACC ATG CAG AAC TAC CTG GTA TGG CGC CTG GTG
leu asp arg ile gly ser leu ser gln arg phe lys glu ala arg val asp tyr arg lys ala leu tyr gly thr thr val glu glu val
1171 CTA GAT CGA ATT GGC AGC CTG AGC CAG AGA TTC AAA GAG GCG CGT GTG GAC TAC CGC AAG GCG CTG TAC GGC AGC ACC GTG GAG GAG GTA
arg trp arg glu cys val ser tyr val asn ser asn met glu ser ala val gly ser leu tyr ile lys arg ala phe ser lys asp ser
1261 CGC TGG CGA GAG TGT GTC AGC TAT GTC AAC AGT AAC ATG GAG AGC GCC GTG GGC TCC CTC TAC ATC AAG CGG GCC TTC TCC AAG GAC AGC
lys ser thr val arg glu leu ile glu lys ile arg ser val phe val asp asn leu asp glu leu asn trp met asp glu glu ser lys
1351 AAG AGC ACG GTC AGA GAG CTG ATT GAG AAG ATA AGG TCC GTG TTT GTG GAT AAC CTG GAG CTG AAC TGG ATG GAC GAG GAA TCC AAG
lys lys ala gln glu lys ala met asn ile arg glu gln ile gly tyr pro asp tyr ile leu glu asp asn asn lys his leu asp glu
1441 AAG AAG GCC CAG GAA AAG GCC ATG AAT ATA CGG GAA CAG ATT GGC TAC CCT GAC TAC ATT TTG GAA GAT AAC AAT AAA CAC CTG GAT GAG
glu tyr ser ser leu thr phe tyr glu asp leu tyr phe glu asn gly leu gln asn leu lys asn ala gln arg ser leu lys lys
1531 GAA TAC TCC AGT TTG ACT TTC TAT GAG GAC CTG TAT TTT GAG AAC GGA CTT CAG AAC CTC AAG AAC AAT GCC CAG AGG AGC CTC AAG AAG
leu arg glu lys val asp gln asn leu trp ile ile gly ala ala val val asn ala phe tyr ser pro asn arg asn gln
1621 CTT CGG GAA AAG GTG GAC CAG AAT CTC TGG ATC ATC GGG GCT GCA GTG GTC AAT GCA TTC TAC TCC CCA AAC AGA AAC CAG ATC GTC TTT

FIG - 3 (cont'd)

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FILE - 3 (cont'd)

2925 TTC

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Sequence of NL-2 cDNA from humans

1 GTG GGG met val glu ser ala gly arg ala gly gln lys arg pro gly phe leu glu gly gln leu leu leu leu leu leu val thr 28
 ala ala leu val ala leu gly val leu tyr ala asp arg arg gly lys gln leu pro arg leu ala ser arg leu cys phe leu gln glu 58
 91 GCT GCC CTG GTG GCC TTG GGT GTC CTC TAC TCC GAC CGC AGA GGG AAG CAG CTG CCA CGC CTT GCT AGC CGG CTG TGC TTC TTA CAG GAG
 glu arg thr phe val lys arg lys pro arg gly ile pro glu ala gln glu val ser glu val cys thr thr pro gly cys val ile ala 88
 181 GAG AGG ACC TTT GTA AAA CGA AAA CCC CGA GGG ATC CCA GAG GCC CAA GAG GTG AGC GAG GTC TGC ACC ACC CCT GGC TGC GTG ATA GCA
 ala ala arg ile leu gln asn met asp pro thr thr thr thr gln phe ala cys gly gly trp leu arg arg his 118
 271 GCC GCC AGG ATC CTC CAG AAC ATG GAC CCG ACC CCG GAA CCG TGT GAC GAC TTC TAC CAG TTT GCA TGC GGA GGC TGG CTG CGG CAC
 val ile pro glu thr thr thr thr thr thr thr thr thr thr thr thr thr thr thr thr thr thr thr thr thr thr thr thr thr 148
 361 GTG ATC CCT GAG ACC AAC TCA AGA TAC AGC ATC TTT GAC GTC CTC CTC GGC GAC GAG CTG GAG GTC ATC CTC AAA GCG GTG CTG GAG AAT TCG
 thr ala lys asp arg pro ala val glu lys ala arg thr leu tyr arg ser cys met asn gln ser val ile glu lys arg gly ser gln 178
 451 ACT GCC AAG GAC CGG CCG GCT GTG GAG AAG GCC AGG ACC GTG TAC CGC TCC TGC ATG AAC CAG AGT GTG ATA GAG AAG CGA GGC TCT CAG
 pro leu leu asp ile leu glu val val gly gly trp pro val ala met asp arg trp asn glu thr val gly leu glu trp glu glu 208
 541 CCC CTG CTG GAC ATC TTG GAG GTG GTG GGA GGC TGG CCG GTG GCG ATG GAC AGG TGG AAC GAG ACC GTA GGA CTC GAG TGG GAG CTG GAG
 arg gln leu ala leu met asn ser gln phe asn arg arg val leu ile asp leu phe ile trp asn asp asp gln asn ser ser arg his 238
 631 CGG CAG CTG GCG CTG ATG AAC TCA CAG TTC AAC AGG CGC GTC CTC ATC GAC CTC TTC ATC TGG AAC GAC GAC CAG AAC TCC AGC CGG CAC
 ile ile tyr ile asp gln pro thr leu gly met pro ser arg glu tyr phe asn gly gly ser asn arg lys val arg glu ala tyr 268
 721 ATC ATC TAC ATA GAC CAG CCC ACC TTG GGC ATG CCC TCC CGA GAG TAC TAC TTC AAC GGC GGC AGC AAC CGG AAG GTG CGG GAA GCC TAC
 leu gln phe met val ser val ala thr leu leu arg glu asp ala asn leu pro arg asp ser cys leu val gln glu asp met val gln 298
 811 CTG CAG TTC ATG GTG TCA GTG GCC ACG TTG CTG CGG GAG GAT GCA AAC CTG CCC AGG GAC AGC TGC CTG GTG CAG GAG GAC ATG GTG CAG 328

715 - 4

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val leu glu leu glu thr gln thr gln ala lys ala thr val pro gln glu glu arg his asp val ile ala leu tyr his arg met gly leu
901 GTT CTG GAG CTG GAG ACA CAG CAG CTG GCC AAG GGC ACC GTC ACC GTC ATC GCC TTG TAC CAC CGG ATG GGA CTG 358
glu glu leu gln ser gln phe gly leu lys gly phe asn trp thr leu phe ile gln thr thr val lys ile lys leu leu
991 GAG GAG CTG CAA AGC CAG TTT GGC CTG AAG GGA TTT AAC TGG ACT CTG TTC ATA CAA ACT GTG CTA TCC TCT GTC AAA ATC AAG CTG CTG 358
pro asp glu glu val val val tyr gly ile pro tyr leu gln asn leu glu asn ile ile asp thr tyr ser ala arg thr ile gln asn
1081 CCA GAT GAG GAA GTG GTG GTC TAT GGC ATC ACC CCC TAC CTG CAG AAC CTT GAA AAC ATC ATC GAC ACC TAC TCA GCC AGG ACC ATA CAG AAC 418
tyr leu val trp arg leu val leu asp arg ile gly ser leu ser gln arg phe lys asp thr arg val asn tyr arg lys ala leu phe
1171 TAC CTG GTC TGG CGC CTG GTG CTG GAC CGC ATT GGT AGC CTA AGC CAG AGA TTC AAG GAC ACA CGA GTG AAC TAC CGC AAG GCG CTG TTT 418
gly thr met val glu glu val arg trp arg glu cys val gly tyr val asn ser asn met glu asn ala val gly ser leu tyr val arg
1261 GGC ACA ATG GTG GAG GAG GTG CGC TGG CGT GAA TGT GTG GGC TAC GTC AAC AGC AAC ATG GAG AAC GCC GTG GGC TCC CTC TAC GTC AGG 478
glu ala phe pro gly asp ser lys ser met val arg glu leu ile asp lys val arg thr val phe val glu thr leu asp glu leu gly
1351 GAG GCG TTC CCT GGA GAC AGC RAG AGC ATG GTC ACA GAA CTC ATT GAC AAG GTG CGG ACA GTG TTT GTG GAG ACG CTG CAC GAG CTG GGC 508
trp met asp glu glu ser lys lys lys ala gln glu lys ala met ser ile arg glu gln ile gly his pro asp tyr ile leu glu glu
1441 TGG ATG GAC GAG TCC AAC AAG AAG GCG CAG CAG GAG AAC GCC ATG AGC ATC CGG GAG CAG ATC GGG CAC CCT GAC TAC ATC CTG GAG GAG 538
met asn arg arg leu asp glu glu tyr ser asn leu asn phe ser glu asp leu tyr phe glu asn ser leu gln asn leu lys val gly
1531 ATG AAC AGG CGC CTG GAC GAG GAG TAC TCC AAT CTG AAC TTC TCA GAG GAC CTG TAC TTT GAG AAC AGT CTG CAG AAC CTC AAG GTG GGC 568
ala gln arg ser leu arg lys leu arg glu lys val asp pro asn leu trp ile ile gly ala ala val val asn ala phe tyr ser pro
1621 GCC CAG CGG AGC CTC AGG AAG CTT CGG GAA AAG GTG GAC CCA AAT CTC TGG ATC ATC GGG GCG GCG GTG GTC AAT CGG TTC TAC TCC CCA 598
asn arg asn gln ile val phe pro ala gly ile leu gln pro pro phe phe ser lys glu gln pro gln ala leu asn phe gly gly ile
1711 AAC CGA AAC CAG ATT GTA TTC CCT GCC GGG ATC CTC CAG CCC TTC AGC AAG GAG CAG CCA CAG GCC TTG AAC TTT GGA GGC ATT 628

SECRET - 4 (cont'd)

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gly met val ile gly his glu ile thr his gly phe asp asp asn gly arg arg asn phe asp lys asn gly asn met met asp trp trp ser
 1801 GGG ATG GTG ATC GGG CAC GAG ATC ACG CAC GGC TTT GAC GAC AAT GGC AAT GGC AAC ATG ATG GAT TGG TGG AGT 658
 asn phe ser thr gln his phe arg glu phe arg glu asn ile tyr gln thr gly asn tyr ser trp asp leu ala asp glu gln asn
 1891 AAC TTC TCC ACC CAG CAC TTC CGG GAG CAG TCA GAG TGC ATG ATC ATC GGC AAC TAC TCC TGG GAC CTG GCA GAA CAG AAC 688
 val asn gly phe asn thr leu gly glu asn ile ala asp asn gly gly val arg gln ala tyr lys leu lys trp met ala glu
 1981 GTG AAC GGA TTC AAC ACC CTT GGG GAA AAC ATT GCT GAC AAC GGC AAC TAT AAG GCC TAC CTC AAC TGG ATG GCA GAG 718
 gly gly lys asp gln gln leu pro gly leu asp thr his glu gln leu phe phe ile asn tyr ala gln val trp cys gly ser tyr
 2071 GGT GGC AAG GAC CAG CAG CTG CCC GGC CTG GAT CTC ACC CAT GAG CAG CTC TTC TTC ATC AAC TAT GCC CAG GTG TGG TGC GGG TCC TAC 748
 arg pro glu phe ala ile gln ser ile lys thr asp val his ser pro leu lys tyr arg val leu gly ser leu gln asn leu ala ala
 2161 CGG CCC GAG TTC GCC ATC CAA TCC ATC AAG ACA GAC GTC CAC CAC ACT CCC CTG AAG TAC AGG GTA CTG GGG TCG CTG CAG AAC CTG GCC GCC 770
 phe ala asp thr phe his cys ala arg gly thr pro met his pro lys glu arg cys arg val trp ter
 2251 TTC GCA GAC ACG TTC CAC TGT GCC CGG GGC ACC CCC ATG CAC CCC AAG GAG CGA TGC CGC GTG TGG TAG CCA AGG CCC TGC CGC GCT GTG
 2341 CGG CCC ACG CCC ACC CGC TGC TCG GAG GCA TCT GTG CGA AGG TGC AGC TAG CGG CGA CCC AGT GTA CGT CCC GCC CCG GCC AAC CAT GCC
 2431 AAG CCT GCC TGC CAG GCC TCT GCG CCT GGC CTA GGG TGC AGC CAC CTG CCT GAC ACC CAG GGA TGA GCA GTG TCC AGT GCA GTA CCT GGA
 2521 CCG GAG CCC CCT TCA CAG ACA CCC GCG GGC CTC AGT GCC CCC GTC ACA ACT CTG TAG AGA CAA TCA ACT GTG TCC TGC CCA CCC TTC AAG
 2611 GTG CAT TGT CTT CCA GTA TCT ACA GCT TCA GAA CTT GAG CTA AGT AAA TGC TTT CAA AGA AAA AAA

FF - 4 (cont'd)

[illegible]

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1171 ile thr val ser glu tyr asp asp leu arg arg asp val ser ser met tyr asn lys val thr leu gly gln leu gln lys ile thr pro
 1261 his leu arg trp lys trp leu leu asp gln ile phe gln glu asp phe ser glu glu glu val val leu leu ala thr asp tyr met
 1351 gln gln val ser gln leu ile arg ser thr pro his arg val leu his asn tyr leu val val val val leu ser glu his
 1441 leu ser pro pro phe arg glu ala leu his glu leu ala gln glu met glu gly ser asp lys pro gln glu leu ala arg val cys leu
 1531 gly gln ala ala asn arg his phe gln met ala leu gly ala leu phe val his glu his phe ser ala ala ser lys ala lys val gln
 1621 leu val glu asp ile lys tyr ile leu gly gln arg leu glu leu asp trp met asp ala glu thr arg ala ala arg ala lys
 1711 leu gln tyr met met val met val gln tyr pro asp phe leu leu lys pro asp ala val asp lys glu phe glu val his glu
 1801 lys thr tyr phe lys asn ile leu asn ser ile arg phe ser ile gln leu ser val lys lys ile arg gln glu val asp lys ser thr
 1891 trp leu leu pro pro gln ala leu asn ala tyr tyr leu pro asn lys asn gln met val phe pro ala gly ile leu gln pro thr leu
 1981 tyr asp pro asp phe pro gln ser leu asn tyr gln gly ile gln thr ile ile gln his glu leu thr his gly tyr asp asp trp gly
 TAC GAC CCT GAC TTC CCA CAG TCT CTC AAC TAC GGC GGC ATC GGC ACC ATC ATT GGA CAT GAG CTG ACC CAC GGC TAC GAC TGG GGG
 652

FRS - 5 (cont'd)

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gly gln tyr asp arg ser gly asn leu leu his trp trp thr glu ala ser tyr ser arg phe leu arg lys ala glu cys ile val arg
2071 GGC CAG TAT GAC GAC CGC TCA GGC AAC CTG CTG CAC TGG TGG ACG AGG GCC TCC TAC ACC CGC TTC CTG CGA AAG GCT GAG TGC ATC GTC CGT
leu tyr asp asn phe thr val tyr asn gln arg val asn gly lys his thr leu gly glu asn ile ala asp met gly gly leu lys
2161 CTC TAT GAC AAC TTC ACT GTC TAC AAC CAG CCG GAG AAC GGG AAA CAC ACG CTT GGG GAG AAC ATC GCA GAT ATG GGC GGC CTC AAG CTG
ala tyr his ala tyr gln lys trp val arg glu his pro glu his pro leu pro arg leu lys tyr thr his asp gln leu phe phe
2251 GCC TAC CAC GCC TAT CAG AAG TGG CTG CCG GAG CAC GGC CCA GAG CAC CCA CTT CCC CGG CTC AAG TAC ACA CAT GAC CAG CTC TTC TTC
ile ala phe ala gln asn trp cys ile lys arg arg ser gln ser ile tyr leu gln val leu thr asp lys his ala pro glu his
2341 ATT GCC TTT GCC CAG AAC TGG TGC ATC AAG CCG CGG TCG CAG TCC ATC TAC TAC CAG CTG CTG ACT GAC AAG CAT GCC CCT GAG CAC TAC
arg val leu gly ser val ser gln phe glu glu phe gly arg val leu his cys pro lys val ser pro met asn pro ala his lys cys
2431 AGG GTG CTG GGC AGT GTG TCC CAG TTT GAG GAG TTT GGC CGG GTT TTA CAC TGT CCA AAG GTC TCA CCC ATG AAC CCT GCC CAC AAG TGT
ser val trp ter
2521 TCC GTG TGG TGA CCC TGG CTG CCC GCC TGC ACG CCC CCA CTG CCC CCG CAC GAA TCA CCT CCT GCT GGC TAC CGG GGC AGG CAT GCA CCC
2611 GGT GCC AGC CCC GGT CTG GGC ACC ACC TGC CTT CCA GCC CCT CCA GGA CCC GGT CCC CCT GGT GGC CCT CAC TTC AGG AGG GGC CTG GAG
2701 CAG GGT GAG GCT GGA CTT TGG GGG GCT GTG AGG GAA ATA TAC TGG GGT CCC CAG ATT CTG CTC TAA GGG GGC CAG ACC CTC TGC CAG GCT
2791 GGA TTG TAC GGG CCC CAC CTT CGC TGT GTT CTT GCT GCA AGT CTG GTC AAA TAA ATC ACT GCA CTG TTA AAA AAA AAA

FILE - 5 (cont'd)

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Sequence comparison between NEP, NL1, NL2 and NL3

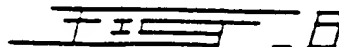
	1	10	20	30	40
NEP-HUM	MG.....	KSESQMDITDINTPKPKKKQ	RWTPLEISLSVLVLL..	LTII...AV	
NL1-MOU	MV.....	ERAGWCRKKS	PGFVEYGLMVLLLLLL	GAIIVTLG.V..	FYSI.GKQL
NL2-HUM	MV.....	ESAGRAGQKR	PGFLEGGLLLLLL	VTAALVALGVL..	YADRRGKQL
NL3-HUM	MEPPYSLTAHYDEFQEVKYVSR	CGAGGARGASLPP	GGFPLGAARSATGARSGL	PRWNRREV	

	50	60	70
NEP-HUM	TMIA.....	LYATYDD.....	GICKSSDCIKSAARLIQ.NMDATT
NL1-MOU	PLLTSL.....	LHFSWDERTVVKR...ALRDSSLKSDICTTPSCVIAAARILE.NMDQSR	
NL2-HUM	PRLASR.....	LCFLQEERTFVKRKRPGIPEAQEVSEVCTTPGCVIAAARILQ.NMDPTT	
NL3-HUM	CLLSGLVFAAGLCAILAAMLALKYLGPVAAGGGACPEGC	PERKAFARAARFLAANLDASI	

	80	90	100	110	120	130
NEP-HUM	EPCTDFFKYACGGWLKRN	VIPETSSRYGNFDILRDELEVVLKDVLPQEPKTEDIVAVQ.KA				
NL1-MOU	NPCENFYQYACGGWLRHH	VIPETNSRYSVFDILRDELEVILKGVLEDSTSQHRPAVE.KA				
NL2-HUM	EPCDDFYQFACGGWLRRH	VIPETNSRYSIFDVLRDELEVILKAVLENSTAKDRPAVE.KA				
NL3-HUM	DPCQDFYSFACGGWLRRAI	PDDKLTYGTIAAIGE	QNEERLRRLRLARPGGGPGGAAQRKV			

	140	150	160	170	180	190
NEP-HUM	KALYRSCINESAIDSRGGE	PLLKLLPDIYGW	PVATENWEQKYGASWTA	EKAIAQLNSKYG		
NL1-MOU	KTLYRSCMNQSVIEKRDSE	PLLSVLKMGVGGWPV	AMDKWNETMGLKWELERQ	LAVLNSQFN		
NL2-HUM	RTLYRSCMNQSVIEKRG	SQPLLDILEVVGW	PVAMDRWNETVGLEWELERQ	LALMNSQFN		
NL3-HUM	RAFFRSCLDMREIERLGP	PRPMLEVI	EDCGGWDLGGAERPGVAARWDLN	RLLLYKAQGVYS		

	200	210	220	230	240	250
NEP-HUM	KKVLINLFVGTDDKNSVN	HVIHIDQPRGLPSRDY	ECTGIYKEACTAYVDFMIS	VARLI		
NL1-MOU	RRVLIDLFIWNDDQNSSRH	VIYIDQPTLGMP	SREYFFQEDNNHKVRKAY	LEFMTSVATML		
NL2-HUM	RRVLIDLFIWNDDQNSSRH	IYIDQPTLGMP	SREYFFNGGSNRKVREAY	LQFMVSVATLL		
NL3-HUM	AAALFSLTVSLDDRNS	SRVIRIDQDGLTLP	ERTLYLAQDEDSE..	KVLAAYRVFMERVL		



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260 270 280 290 300 310
 NEP-HUM RQEERLPIDENQLALEMKNVMELEKEIANATAKP..EDRNDPMLLYNKMTLAQIQNNFSL
 * * * * *
 NL1-MOU RKDQNL SKESAMVREEMA EVLELETHLANATVPQ..EKRHDVTALYHRMDLMELQERFGL
 * * * * *
 NL2-HUM REDANLPRDSCLVQEDMVQVLELETQLAKATVPQ..EERHDVIALYHRMGLEELQSQFGL
 * * * * *
 NL3-HUM SL...LGADAV..EQKAQEILQVEQQLANITVSEYDDLRRDVSSMYNKVTLGQLQKITP.

320 330 340 350 360 370
 NEP-HUM EINGKPF SWLNFTNEIMSTVNISITNEEDVVVYAPEYLT KLKPI LTKYSARDLQNLMSWR
 * * * * *
 NL1-MOUKGFNWT LFIQNV LSSVEVELFPDEEV VVGIPYLENLEDIIDSYSARTMQNYLVWR
 * * * * *
 NL2-HUMKGFNWT LFIQTV LSSVKIKLLPDEEV VVGIPYLQNLNIIDTYSARTIQNYLVWR
 * * * * *
 NL3-HUMHLRWK WLLDQIF...QEDFSEEEEVVLLATDYMQQVSQLIRSTPHRVLHNYLVWR

380 390 400 410 420 430
 NEP-HUM FIMDLVSSLSR TYKESRNAFRKALYGT TSETATWRR CANYVNGN MENAVGR LYEAA FAG
 * * * * *
 NL1-MOU LVLDRIGSLSQR FKEARVDYRKALYGT TVEEVRWREC VSYVNSNMESAVGSLYIKRAF SK
 * * * * *
 NL2-HUM LVLDRIGSLSQR FKDTRVNYRKALFG TMVEEVRWREC VGYVNSNMENAVGSLYVREAF PG
 * * * * *
 NL3-HUM VVVVLSEHLSPP FREALHELAQEMEGSDKPQELARVCLGQANRHF GMALGALFVHEHFSA

440 450 460 470 480 490
 NEP-HUM ESKHVVEDLIAQIREVFIQT LDDLTWMDAETKKRAEEKALAIKERIGYPDDIVSNDNK.L
 * * * * *
 NL1-MOU DSKSTVRELIEKIRSVFVDNLDELNWMDEESKKKAQEKAMNIREQIGYDPDYILEDNNKHL
 * * * * *
 NL2-HUM DSKSMVRELIDKVRTVFVETLDELGWMDEESKKKAQEKAMSIREQIGHDPDYILEEMNRRL
 * * * * *
 NL3-HUM ASKAKVQQLVEDIKYILGQRLEELD WMDAETRAAARAKLQYMMVMVGYPD FLLKPD A..V

500 510 520 530 540 550
 NEP-HUM NNEYLELNYKEDEYFENIIQNLKFSQSKQLKKLREKVDKDEWISGA AVVNAFYSSGRNQI
 * * * * *
 NL1-MOU DEEYSSLTFYEDLYFENGLQNLKNN AQRSLKKLREKVDQNLWII GA AVVNAFYSPNRNQI
 * * * * *
 NL2-HUM DEEYSNLNFSEDLYFENSLQNLKVGAQRSLRKLREKVDPNLWII GA AVVNAFYSPNRNQI
 * * * * *
 NL3-HUM DKE.YEFEVHEKTYFKNI LNSIRFSIQLSVKKIRQEVDKSTWLLPPQALNAYYLPNKNQM

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560 570 580 590 600 610
 NEP-HUM VFPAGILQPPFFSAQQSNLSNYGGIGMVIGHEITHGFDDNGRNFNKGDLVDWWTQQSAS

 NL1-MOU VFPAGILQPPFFSKDQPQSLNFGGIGMVIGHEITHGFDDNGRNFNKGDLVDWWTQQSAS

 NL2-HUM VFPAGILQPPFFSKEQPQALNFGGIGMVIGHEITHGFDDNGRNFNKGDLVDWWTQQSAS

 NL3-HUM VFPAGILQPTLYDPDFPQSLNYGGIGTIIGHELTHGYDDWGGQYDRSGNLLHWWTEASYS

620 630 640 650 660 670
 NEP-HUM NFKEQSQCMIYQYGNFSWDLAGGQHLNGINTLGENIADNGGLGQAYRAYQNYIKKNGEEK

 NL1-MOU HFQQQSQCMIYQYGNFSWELADNQNVNGFSTLGENIADNGGVRQAYKAYLRWLADGGKQDQ

 NL2-HUM HFREQSECMYQYGNYSWDLADEQNQNVNGFNTLGENIADNGGVRQAYKAYLKWMAEGGKQDQ

 NL3-HUM RFLRKAECIVRLYDNFT...VYNQVRNGKHTLGENIADMGGGLKLAYHAYQKWVREHGPEH

680 690 700 710 720 730
 NEP-HUM LLPGLDLNHHKQLFFLNFAQVWCGTYRPEYAVNSIKTDVHSPGNFRIIGTLQNSAEFSEAF

 NL1-MOU RLPGLNLTIAQLFFINIAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQNLPGFSEAF

 NL2-HUM QLPGLDLTHEQLFFINIAQVWCGSYRPEFAIQSIKTDVHSPLKYRVLGSLQNLAAAFADTF

 NL3-HUM PLPRLKYTHDQLFFIAFAQNWCICKRRSQSIYLQVLTDKHAPEHYRVLGSLVSVQFEEFGRVL

740 750
 NEP-HUM HCRKNSYMNPEKKCRVW

 NL1-MOU HCPRGSPMHPMKRCRIW

 NL2-HUM HCARGTPMHPKERCVRW

 NL3-HUM HCPKVSPMNPAAHKCSVW

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NL1 in the TESTIS

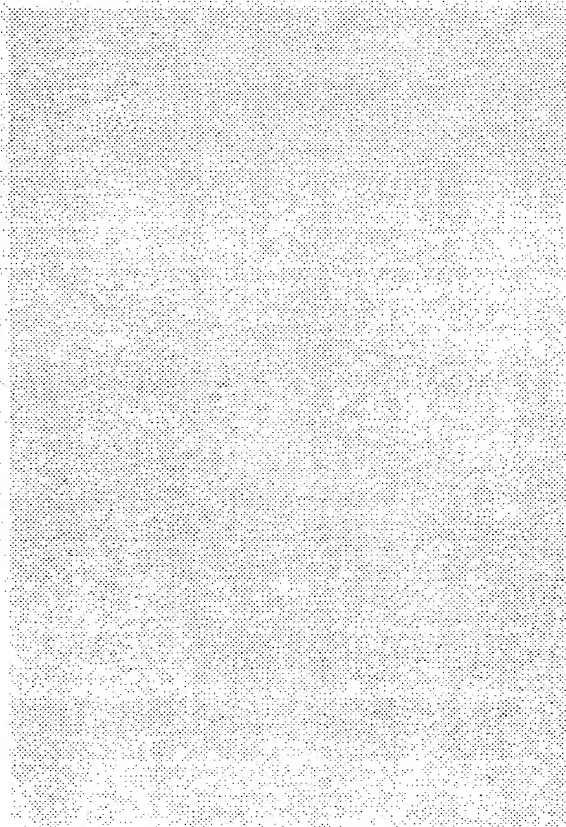
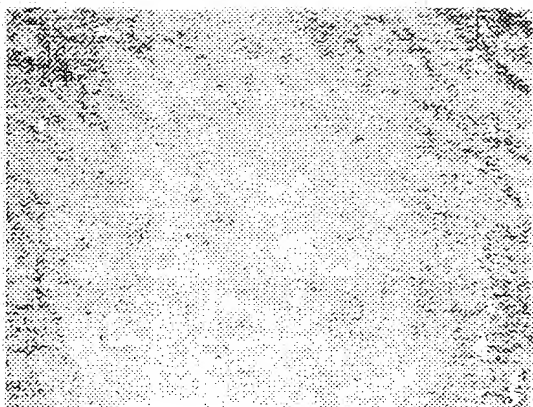
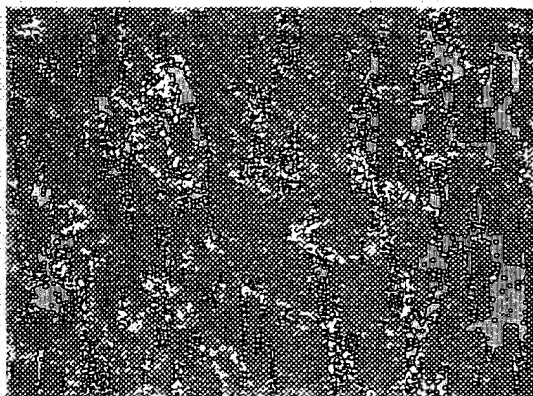


FIG. 7

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FIG. 7

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Expression of PEX and NL-3 in normal and Hyp mouse embryos

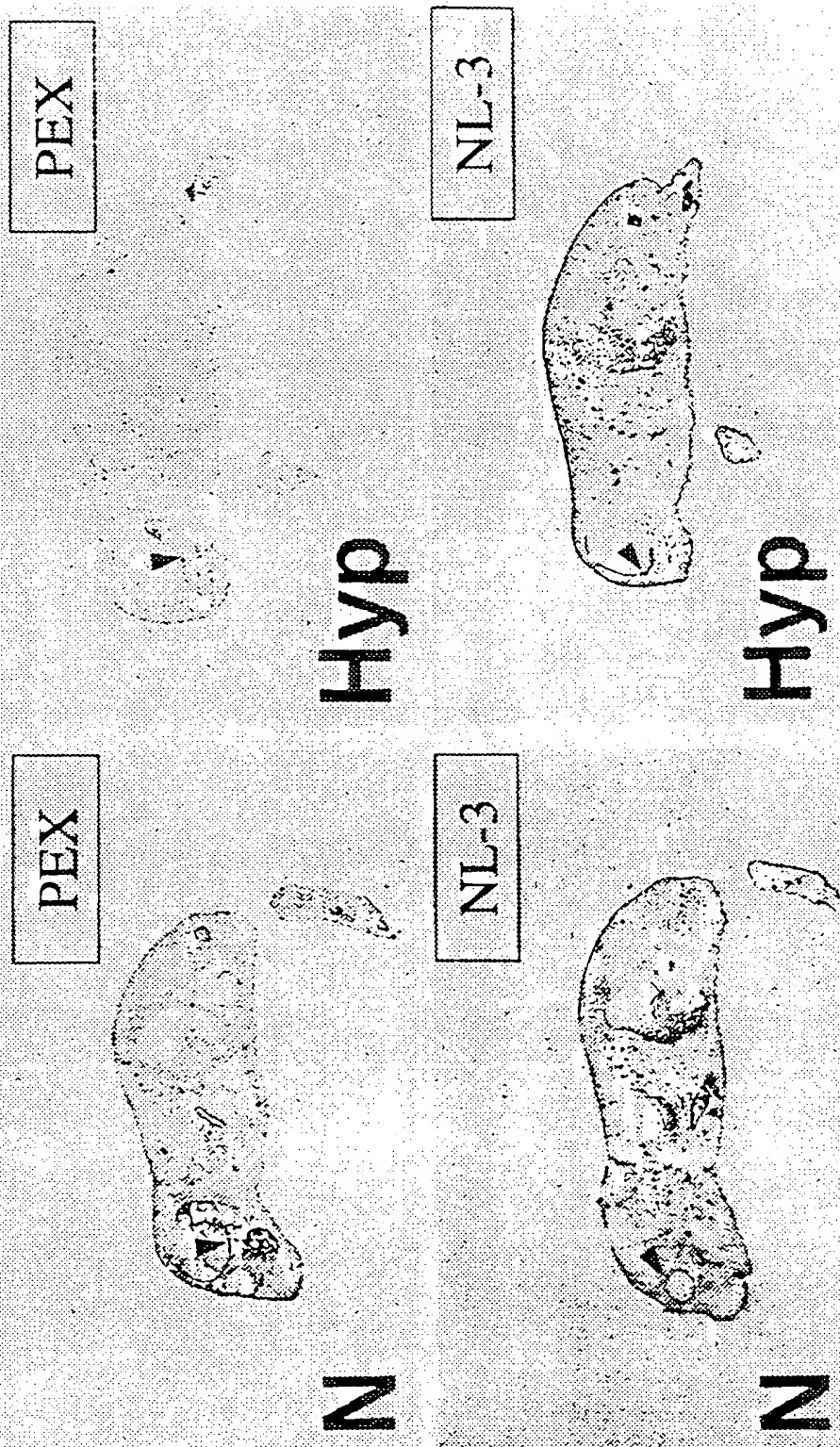
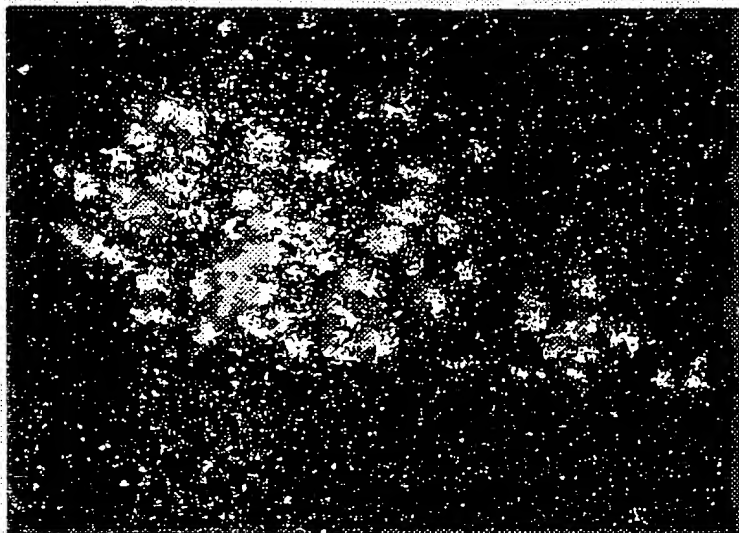


FIG. 8

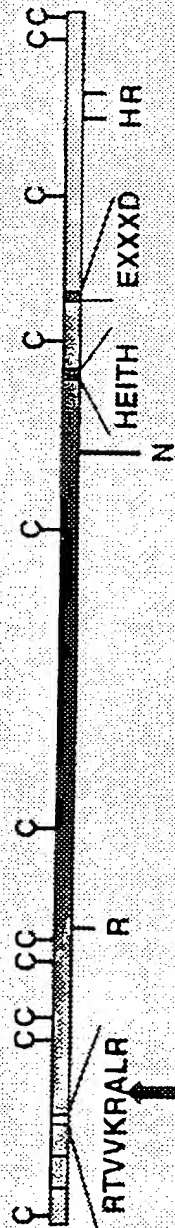
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NL3 in the BRAIN



0913329.082101

Structure and expression of NL-1



Northern blot

heart
brain
spleen
lungs
liver
skel. muscle
testis
kidney

3.4 kb →

Western blot of transfected CHO cells

Mock
Untreated
Endo H
PNGase F

116 kDa
87 kDa

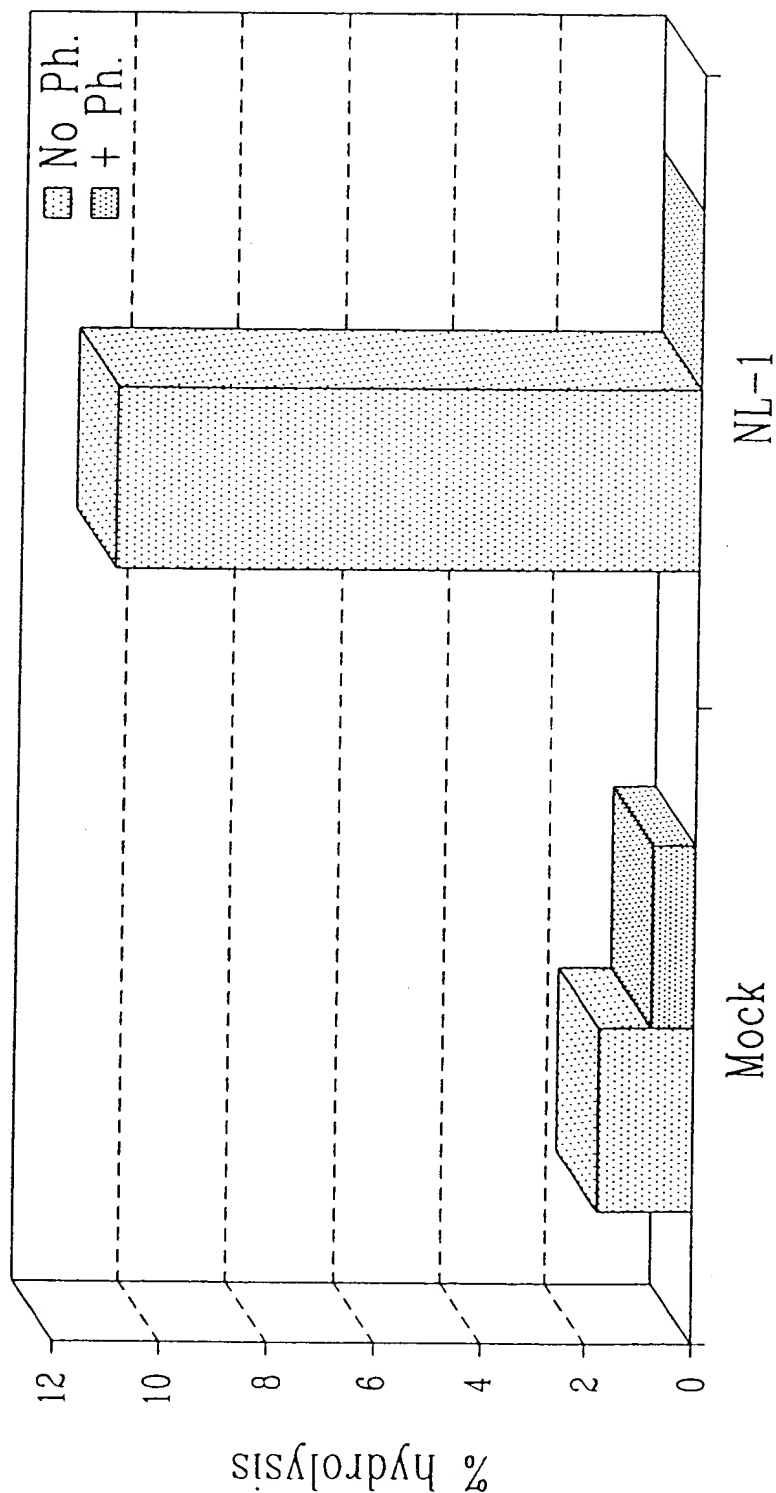
FIG. 10

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Enzymatic activity of NL-1



Degradation of [³H]Tyr, D-Ala₂, Leu₅-enkephalin

Fig. 11

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MOCK NL-3 CTL NL-3

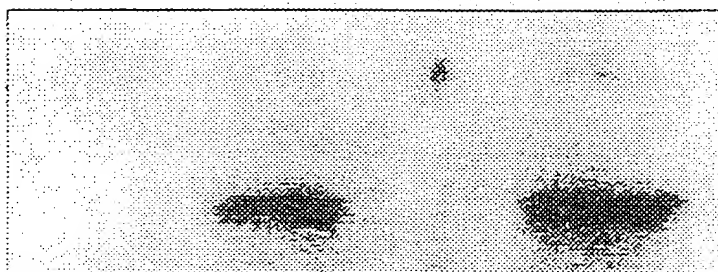


FIG. 12